

# SEQUENCE LISTING

<110> LUKYANOV, SERGI A  
SHAGIN, DMITRY A  
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA  
HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10/532,681

<141> 2005-04-26

<160> 22

<170> PatentIn version 3.3

<210> 1

<211> 784

<212> DNA

<213> phialidium sp

<400> 1  
gaactgataa aagaaatcat catcatgtct agtggagcac tgttggtcca cgaaagatc 60  
ccatatgttg ttgagatgga gggaaatggt gatggacaca cattctccat tagaggtaaa 120  
ggttatggag atgcaagtgt tggtaaagtt gatgcccaat tcatctgcac aactggagat 180  
gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc 240  
aaatatggtc cagaattaaa ggatttctac aagagttgca tgcctgaagg ctatgtgcag 300  
gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctgcgcgtga agttacattt 360  
gaaaacggat ctgtttataa ccgagtcaaa cttaatggac aaggatttaa gaaagacgga 420  
catgtgcttg gaaagaatct tgaattcaat ttcacacctc attgtcttta catttgggga 480  
gatcaggcta atcatggttt gaagtctgct ttcaaaatta tgcattgagat tactggatca 540  
aaagaagact tcattgttgc agaccacacc caaatgaaca caccattgg tgggtggacca 600  
gtccatgtcc ctgaatacca tcatataaca taccatgtca ctctcagcaa agatgttact 660  
gatcacaggg ataacatgag cttggttgaa accgtacggg ctgtggattg cagaaaaaca 720  
tatctttaaa ttgtaaattt atttgtagtt gaaaaccttt tgtcacgata tataccttta 780  
ttat 784

<210> 2

<211> 234

<212> PRT

<213> Phialidium sp

<400> 2

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 3  
<211> 705  
<212> DNA  
<213> Artificial

<220>  
<223> phiYFP-Y1 mutant of the phiYFP

<400> 3  
atgcctagtg gagcactgtt gttccacgga aagatcccat atgttggtga gatggagggga 60  
aatgttgatg gacacacatt ctccattaga ggtaaagggt atggagatgc aagtgttggt 120  
aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180  
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240  
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300  
gacggagtat ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360

gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa 420  
 ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag 480  
 tctgctttca aaattatgca tgagattact ggatcaaaaag gagacttcat tgttgcagac 540  
 cacacccaaa tgaacacacc cattgggtggg ggaccagtcc atgtccctga ataccatcat 600  
 atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg 660  
 gttgaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 4  
 <211> 234  
 <212> PRT  
 <213> Artificial

<220>  
 <223> phiYFP-Y1 mutant of the phiYFP

<400> 4

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
 1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser  
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

<210> 5  
 <211> 705  
 <212> DNA  
 <213> Artificial

<220>  
 <223> phiYFP-M0 mutant of the phiYFP

<400> 5  
 atgcctagtg gagcactgtt gttccacgga aagatcccat atgttggtga gatggagggg 60  
 aatgttgatg gacacacatt ctccattaga ggtaaagggt atggagatgc aagtgttggt 120  
 aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180  
 gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggtccaga attaaaggat 240  
 ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300  
 gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360  
 gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa 420  
 ttcaatttca cacctcattg tctttacatt tggggagatc aggctaata tggtttgaag 480  
 tctgctttca aaattcgcca tgagattact ggatcaaaaag gagacttcat tgttgcagac 540  
 cacacccaaa tgaacacacc catttggtggg ggaccagtcc atgtccctga aaaccatcat 600  
 atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660  
 aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 6  
 <211> 234  
 <212> PRT  
 <213> Artificial

<220>  
 <223> phiYFP-M0 mutant of the phiYFP

<400> 6

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
 1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 7  
<211> 705  
<212> DNA  
<213> Artificial

<220>  
<223> phiYFP-M1 mutant of the phiYFP

<400> 7  
atgtctagtg gagcactggt gttccacgga aagatcccat atgttggtga gatggagggga 60  
aatgttgatg gacacacatt ctccattaga ggtaaagggt atggagatgc aagtgttggt 120  
aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180  
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240  
ttctacaaga gttgcatgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg 300  
gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360  
gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaat gaatcttgaa 420

ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag	480
tctgctttca aaatttgcca tgagattact ggatcaaaaag gagacttcat tgttgcagac	540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat	600
atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg	660
aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa	705

<210> 8  
 <211> 234  
 <212> PRT  
 <213> Artificial

<220>  
 <223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 9  
<211> 705  
<212> DNA  
<213> Artificial

<220>  
<223> humanized version of the phiYFP-M1

<400> 9  
atgagcagcg gcgccctgct gttccacggc aagatcccct acgtggtgga gatggagggc 60  
aatgtggatg gccacacctt cagcatccgc ggcaagggtc acggcgatgc cagcgtgggc 120  
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180  
gtgaccaccc tgacctacgg cgcccagtg ttcgccaagt acggccccga gctgaaggat 240  
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300  
gatggcaatt tcaagaccgg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360  
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420  
ttcaatttca cccccactg cctgtacatc tggggcgatc aggccaatca cggcctgaag 480  
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540  
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600  
atgagctacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660  
aaggagaccg tgcgcgccgt ggattgccgc aagacctacc tgtga 705

<210> 10  
<211> 234  
<212> PRT  
<213> Artificial

<220>  
<223> humanized version of the phiYFP-M1

<400> 10

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 11  
<211> 1047  
<212> DNA  
<213> Anthomedusae species

<220>  
<221> misc\_feature  
<223> hydromedusa 1 from sub-order Anthomedusae

<400> 11  
cttttcttaa aaagaattca aaaaggacgg tttactagac atacttatac agctttactt 60  
ataaaggaag aaatgaatgt gatgcgttac aacagaggat tctgcagagt ttgcaaaat 120  
gggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaacccgt catacttggt 180  
gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240  
gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tgggtgtaatt 300  
gaaggaaaat atgtttgtac agaaggagaa gttcctatatt catgggtttc gctcatcacc 360  
tcattaagtt atggtgcgaa atgttttggt cgatatccaa atgaaataaa tgattttttc 420



```

aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt 480
gttttagaaa cagcagctaa aattactatg gaaagtgggtg caatagtga tagaataaat 540
gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc 600
cctccttcga caacatatgt tgttcccgag ggagaaggta ttcgaatcat ctatagaaac 660
atctatccaa caaaagatgg tcactatggt gttgccgaca cacagcaagt aaatcgacca 720
attagagcac aaggaacatc agctatccca acatatcatc acattaaatc gaaagttgat 780
ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca 840
tttgacgctg atttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaag 900
ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa 960
tatattttca aataaacttt ataaaattag gaatctttga atatataaac taaacctttt 1020
attttagaa taaaaataat taaagac 1047

```

```

<210> 12
<211> 262
<212> PRT
<213> Anthomedusae species

<220>
<221> MISC_FEATURE
<223> hydromedusa 1 from sub-order Anthomedusae

<400> 12

```

```

Met Asn Val Met Arg Tyr Asn Arg Gly Phe Cys Arg Val Leu Gln Asn
1          5          10          15

```

```

Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro
          20          25          30

```

```

Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
          35          40          45

```

```

Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
          50          55          60

```

```

Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
          65          70          75          80

```

```

Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
          85          90          95

```

```

Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
          100          105          110

```

```

Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
          115          120          125

```

```

Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
          130          135          140

```

Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr  
145 150 155 160

Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser  
165 170 175

Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile  
180 185 190

Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala  
195 200 205

Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala  
210 215 220

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp  
225 230 235 240

Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala  
245 250 255

Phe Asp Ala Asp Phe Ser  
260

<210> 13  
<211> 1089  
<212> DNA  
<213> Anthomedusae species

<220>  
<221> misc\_feature  
<223> hydromedusa 2 from sub-order Anthomedusae

<400> 13  
atcattcgct gatacgaagt gaaagtagcg tttgctgaaa gcttcctgga attgctccta 60  
cgtatcttga aagttgctcc tacgctccaa cttgtttgtt caaaatggaa ggtgggtccag 120  
cattatttca atccgatatg acattcaaga tcttcatcga tggagtgggtg aatgatcaga 180  
aattcacgat aatcgcatg ggatcgcca aattcccca tgggtgacttc aacgtgcatg 240  
ctgtgtgcga aaccgggaaa ctccaatgt catggaaacc tatttgtcac cttatccaat 300  
acgggggagcc attctttgca aaatatccca atggcatcag ccattttgca caggagtgt 360  
ttccagaagg attaacaatt gatcgaacag tcagattcga aaatgacggc actatgacgt 420  
ctcaccacac ctatgagttg gacggcacct gtgtcatttc caggataacc gttaattgtg 480  
acggatttca acctgatgga ccaatcatga aagaccagct tgttgatcgc ctgccaactg 540  
agacacatat gttccctcat ggggtccaatg ctgtcagaca attgtgctac attggcttca 600  
cgacagctga tgggtggtctc atgatgtcac attttgattc gaaattgaca ttcaatgggt 660  
cgagagcaat caagattcct ggacctcatt tcgttactgt gataatcaaa cagatgaaag 720  
atacaagcga caagcgtgat catgtgtgtc aacgtgaagt cacctacgct cactcagttc 780  
cacgcatcac ttctgctatc taaacatcat tcttaaaagg ggaacatgca catcatactt 840

cagtgtgagg gtcagtgtga gggctcttttag atgtcaattt gtcgcagggtg tcacacggcg 900  
 tcgttttagat gttgaaggac gaaatgagac aaagagatta atagagactc atatttttat 960  
 gtagaatcga ttcattcagc ccattggtaa cttttttggt attttatcat cttattattg 1020  
 tattggcact ttgtttatat tttgtatgta atgtgtaaac aattgttgaa aatacatgtc 1080  
 aagaacttg 1089

<210> 14  
 <211> 232  
 <212> PRT  
 <213> Anthomedusae species

<220>  
 <221> MISC\_FEATURE  
 <223> hydromedusa 2 from sub-order Anthomedusae

<400> 14

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile  
 1 5 10 15

Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp  
 20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys  
 35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
 50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His  
 65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val  
 85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
 100 105 110

Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
 115 120 125

Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro  
 130 135 140

Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu  
 145 150 155 160

Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
 165 170 175

Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
 180 185 190

Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser  
 195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
 210 215 220

Val Pro Arg Ile Thr Ser Ala Ile  
 225 230

<210> 15  
 <211> 699  
 <212> DNA  
 <213> Artificial

<220>  
 <223> S3-2 mutant of hm2CP from a hydromedusa 2 of sub-order Anthomedusa

<400> 15  
 atggaagggtg gtccagcatt atttcaatcc gacatgacat tcaagatctt catcgatgga 60  
 gtggtgaatg gtcagaaatt cacgatagtc gcagatggat cgtccaaatt ccccatggt 120  
 gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaaccatt 180  
 tgtcacctta tccaatacgg ggagccattc tttgcaagat atccaacgg catcagccat 240  
 tttgcacagg agtgctttcc agaaggatta tcaattgatc gaacagtcag attcgaaaat 300  
 gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg 360  
 ataaccgtta attgtgacgg atttcaacct gatggaccaa tcatgagaga ccagcttggt 420  
 gatatcctgc caaacgagac acatatgttc cctcatggac ccaatgctgt cagacaattg 480  
 gctttcatag gcttcacgac agctgatggt ggtctcatga tgtcacattt tgattcgaaa 540  
 atgacattca atggttcgag agcaatcaag attcctggac ctcatctcgt cactaccata 600  
 accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc 660  
 tacgtcact cagttccacg catcacttct gctatctaa 699

<210> 16  
 <211> 232  
 <212> PRT  
 <213> Artificial

<220>  
 <223> S3-2 mutant of hm2CP from a hydromedusa 2 of sub-order Anthomedusae

<400> 16

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile  
 1 5 10 15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp  
 20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys  
 35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His  
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val  
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro  
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu  
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile  
225 230

<210> 17  
<211> 705  
<212> DNA  
<213> Artificial

<220>  
<223> phiYFP-M1G1 mutant, derived from humanized version of the  
phiYFP-M1

<400> 17  
atgtccagcg gcgccctgct gttccacggc aagatcccct acgtggtgga gatggagggc 60  
aatgtggatg gccacacctt cagcatccgc ggcaagggtc acggcgatgc cagcgtgggc 120  
aagggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180  
gtgaccaccc tgtcctacgg cgcccgatgc ttcgccaagt acggccccga gctgaaggat 240  
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300

gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360  
 gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420  
 ttcaatttca cccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag 480  
 agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcac cgtggccgat 540  
 cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600  
 atgagcacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660  
 aaggagaccg tgcgcgccgt ggattgccga acagcctacc tgtga 705

<210> 18  
 <211> 234  
 <212> PRT  
 <213> Artificial

<220>  
 <223> phiYFP-M1C1 mutant, derived from humanized version of the  
 phiYFP-M1

<400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu  
225 230

<210> 19  
<211> 705  
<212> DNA  
<213> Artificial

<220>  
<223> phiYFP-M1C1 mutant, derived from humanized version of the  
phiYFP-M1

<400> 19  
atgtccagcg ggcgccagct gttccacggc aagatcccct acgtggtgga gatggagggc 60  
aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120  
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180  
gtgaccaccc tgtcctgggg cgcccagtg ttcgccaagt acggccccga gctgaaggat 240  
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300  
gatggcaatt tcaagaccgc cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360  
gtgaagctga aaggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420  
ttcaatttca cccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag 480  
agcgccttca agatctgcca cgagatcacc ggccagtaagg gcgatttcat cgtggccgat 540  
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600  
atgagcacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660  
aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga 705

<210> 20  
<211> 234  
<212> PRT  
<213> Artificial

<220>  
<223> phiYFP-M1C1 mutant, derived from humanized version of the  
phiYFP-M1

<400> 20

Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val  
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 21  
<211> 699  
<212> DNA  
<213> Artificial

<220>  
<223> humanized version of th S3-2 mutant of hm2cp from a hydromedusa 2  
of sub-order Anthomedusae

<400> 21  
atggagggcg gccccgccct gttccagagc gacatgacct tcaaaatctt catcgacggc 60  
gtggtgaacg gccagaagtt caccatcggt gccgacggca gcagcaagtt cccccacggc 120  
gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc 180  
tgccacctga tccagtacgg cgagcccttc ttcgcccgt accccaacgg catcagccac 240



ttcgcccagg agtgcttccc cgagggcctg agcatcgacc gcaccgtgcg cttcgagaac 300  
 gacggcacca tgaccagcca ccacacctac gagctggacg gcacctgcgt ggtgagccgc 360  
 atcaccgtga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg 420  
 gacatcctgc ccaacgagac ccacatgttc cccacgggcc ccaacgccgt gcgccagctg 480  
 gccctcatcg gcttcaccac cgccgacggc ggcctgatga tgagccactt cgacagcaag 540  
 atgaccttca acggcagccg cgccatcaag atccccggcc cccacttcgt gaccaccatc 600  
 accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc 660  
 tacgcccaca gcgtgccccg catcaccagc gccatctga 699

<210> 22  
 <211> 232  
 <212> PRT  
 <213> Artificial

<220>  
 <223> humanized S3-2 mutant of hm2cp from a hydromedusa 2 of sub-order Anthomedusae

<400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile  
 1 5 10 15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp  
 20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys  
 35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
 50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His  
 65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val  
 85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
 100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
 115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro  
 130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu  
 145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
 165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile  
225 230